

## Belgian 'farm-to-consumption' risk assessment-model for *Salmonella* in pigs: methodology for assessing the quality of data and information sources

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### Abstract

Quantitative Microbiological Risk Assessment (QMRA) is a scientific tool that can be used to evaluate the level of exposure and subsequently the risk to human health. However, using this technique one should be aware of the limits of the QMRA model due to data quality, limited amount of time, model uncertainty and quality of assumptions. In addition, each information source may have different study designs, sampling methods, diagnostic tools, etc. Within the Belgian *Salmonella* QMRA-model in pigs, following exposure pathways were identified: primary production, transport, slaughterhouse & post processing, distribution & storage, consumer, dose response. From more than 60 available data sources, information was available for up to 101 potential input parameters, which were essential for building up the model-framework. For each parameter different specifications were summarised. In order to evaluate the quality of these input parameters and to measure their importance and possible impact on the outcome of the risk assessment model, a NUSAP/Pedigree methodology was chosen. Four different criteria used in the matrix include: proxy representation, empirical basis, methodology and validation. Every input parameter was scored by a panel of experts using these pedigree criteria. The overall scores or strength (aggregate of the 4 criteria) for each parameter was obtained by using appropriate weighted methods. The obtained strengths for each parameter should be taken into account when building the QMRA model. This scoring exercise showed for the first time the use of the NUSAP/Pedigree method as an essential tool in QMRA. It showed to be enhancing the credibility of the model in its communication towards decision makers.

### Introduction

Quantitative microbial risk assessment (QMRA) is a scientifically based process used to evaluate quantitatively the exposure and adverse effects of microorganisms to human health. Often QMRAs rely on poor data with gaps and deficiencies (Gardner, 2004). This article aims to provide a novel approach in assessing the quality of data involved in QMRA. Quality of data is defined here as a measure of the fitness for the purpose for which the data will be used (Southgate, 2002). Gardner (2004) indicates that in microbial risk assessment, quality of data is related to the amount, the completeness, validity, relevance, comparability and timeliness of data, as well as to sampling methods and the use of (imperfect) diagnostic tests. We used a Pedigree assessment to address this problem. It emerged in the context of the Numerical Unit Spread Assessment Pedigree (NUSAP) notational system which aims to provide a better management and communication of uncertainty in science for policy (Funtowicz and Ravetz, 1990). The Pedigree evaluates the scientific underpinning of numbers used in a risk assessment. It is expressed by a set of pedigree criteria in a pedigree matrix. The pedigree matrix is used to code each criterion on a discrete numerical scale from 0 (weak) to 4 (strong). Assessment of pedigree involves qualitative expert judgment (van der Stuijs et al., 2005a).

The Pedigree method was applied to a Belgian farm-to-fork model aiming to assess the risk of *Salmonella* due the consumption of pig meat (Metzoon project). Scoring the parameters with this



method intended a clear documentation and a structured selection of input parameters used for this model.

## Material and methods

Stakeholders of the Metzoon project described following model pathways: primary production, transport slaughterhouse & post processing, distribution & storage, consumer. These pathways form the backbone of the QMRA model, and have to be supplied with available input parameters originating from various sources of information such as epidemiological, observational studies, surveys, (un)published literature and expert opinion. The potential model parameters were specified in an Access database as an ID-card by means of their reference, the used sampling frame (study population, sample size, non-response, diagnostic test,...), information for central tendency, range, and distribution. The pedigree matrix was adapted from van der Sluijs (2005b) and the criteria used to evaluate the parameter strength are summarised in Table 1.

Table 1: Parameter matrix for parameter strength

Score	Proxy	Empirical	Method	Validation
4	Exact measure of the desired quantity (e.g. geographically representative)	Large sample direct measurements, recent data, controlled experiments	Best available practice in well-established discipline (accredited method for sampling / diagnostic test)	Compared with independent measurements of the same variable over long domain, rigorous correction of errors
3	Good fit or measure (measurements used from another geographical area but representative)	Historical/field data, small sample, direct measurements, less recent data, uncontrolled experiments, low non-response rate	Reliable method common within established discipline, best available practice in immature discipline (sampling / diagnostic test)	Compared with independent measurements of closely related variable over shorter period
2	Well correlated but not measuring the same thing (large geographical differences)	Very small sample, historical data, Modelled/derived data / indirect measurements, organised expert elicitation	Acceptable method but limited consensus on reliability of sampling & diagnostic test	Compared with measurements not independent, proxy variable, limited domain
1	Weak correlation (very large geographical differences)	1 Expert opinion, rule of thumb estimate	Preliminary methods with unknown reliability	Weak, very indirect validation
0	Not clearly correlated	Crude speculation	No discernible rigour	No validation

The 101 parameters were scored using the information from the parameter ID-cards by 10 Metzoon experts. The strength of each parameter is calculated taken into account: (a) the expertise of the experts, (b) the consistency in rating between experts and (c) the number of experts actually rating the characteristic. In particular, the strength of a parameter is defined as the mean of the strengths of its pedigree criteria. The latter are calculated as  $S_i = \frac{1}{4} R_i C_i \bar{X}_{\text{weight},i}$  (with  $i = 1, \dots, 4$ ) where (a)  $\bar{X}_{\text{weight},i}$  is a weighted mean of the ratings with the weights reflecting the expertise of the experts, where (b)  $C_i = 1 - s_i/E_i$  with  $s_i$  being the observed standard deviation of the ratings and  $E_i$  is the entropy or the maximal standard deviation possible and where (c)  $R_i = N_i/N$  with  $N_i$  being the number of experts actually rating criterion  $i$  and  $N$  is the number of experts involved in the study ( $N = 10$ ). Finally, note that an alternative (often used) way to account for raters consistency is dividing the mean by its standard deviation. However, when all raters agree, the standard deviation is zero and division by zero leads to undefined results. This problem is avoided when using formula (b).

## Results

The resulting strength of the 101 parameters scored by 10 experts is graphically represented for the different modules in figure 1. The majority of the experts attributed low scores for the validation-criterion, partly because no validation was performed and partly because they were not sure if

there had been a validation of the parameters. We will overview most important examples of parameter strengths.

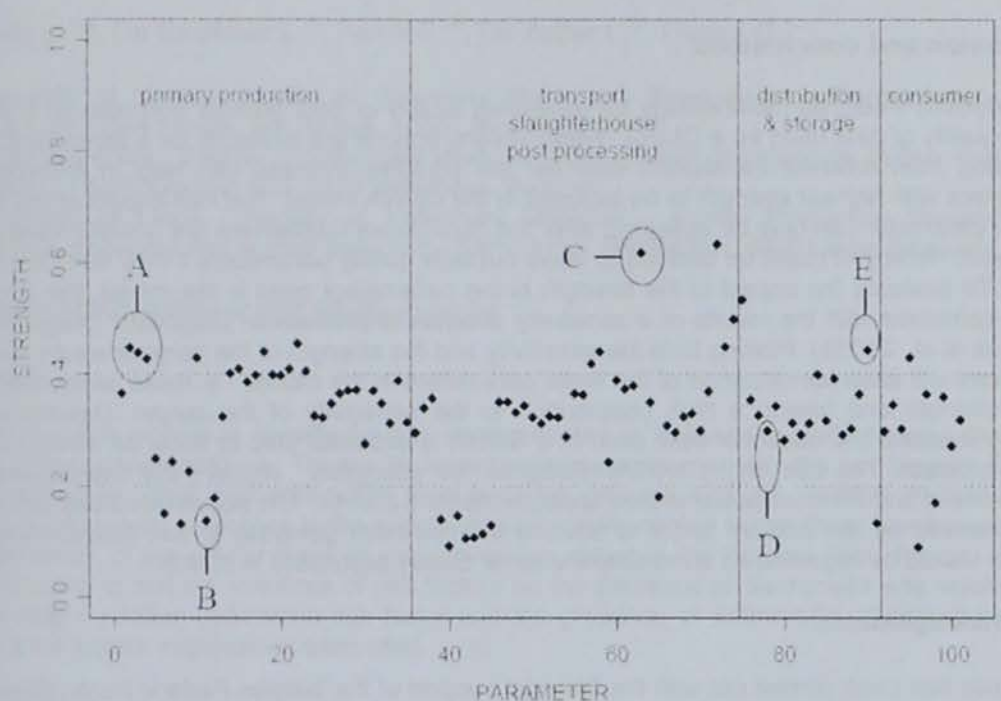


Figure 1: Overall parameter strength distributed according to the production pathways. Scores  $<0.2$  = low strength, between 0.2 and 0.4 = moderate/high strengths,  $>0.4$  = very high strength. A complete legend with definitions of the represented parameter numbers (1-101) can be obtained from the first author.

High parameter strengths were attributed to parameters representing the prevalence of *Salmonella* spp. in pig feed (figure 1, A). The data used to estimate these parameters were provided by an association of feed producers and by the Belgian Federal Agency for the Safety of the Food Chain (FASFC). These parameters obtained very high scores for the proxy criterion, and moderate to high scores for the criteria empirical rigour and methodology. This is due to the fact that the values are considered representative for the Belgian situation, sufficiently recent, obtained by a large sample size and that a coherent sampling methodology as well as a good diagnostic test procedure was used throughout to obtain the data. The parameter B in figure 1 represents the duration of shedding of *Salmonella* Typhimurium & *Choleraesuis* in pig. The low strength of this parameter can be explained by a low score for the proxy criterion, because the duration of shedding was estimated from population of pigs in the USA, using the *Choleraesuis* serotype which is not common in the Belgian pig population. Low empirical scores resulted from the use of indirect aggregated measurements from different studies. In addition, low scores were given for the methodological rigour and scores for validation. Within the slaughterhouse & post processing module (figure 1, C), the parameter estimating the prevalence of *Salmonella* spp. at the end of the slaughter line (provided by the FASFC) was attributed a high parameter strength. Next to very high scores for proxy, empirical basis, methodological rigour, the parameter was also considered as sufficiently validated. The data could be validated with *Salmonella* prevalence data originating from private companies. Concerning the distribution & storage module, a number of parameters were obtained through questionnaires (figure 1, D). The parameter "duration of pig carcass storage in the storage room" (D, figure 1) obtained a moderate strength. Hereby, the empirical basis did not reach very high scores, due to the fact that values were obtained indirectly by means of an oral interview with the quality managers from the cutting plant visited instead of measurement by the interviewers themselves. The experts gave high scores to the parameter estimating the temperature of pig meat in the fridge (E, figure 1). This parameter was obtained through a national Belgian Food Consumption Survey among 3001 households. Although the temperature was not



measured in the pork meat itself, but in the lowest drawer of the fridge, it still yielded a high proxy score. Likewise, the empirical basis (due large sample size and direct measurements), and the methodological rigour received very high scores.

## Discussion and conclusions

The proposed Pedigree methodology for assessing quality of data permits a structured reflection on the quality of data used for a QMRA. When several options are available for a same parameter, originating from different information sources, the pedigree process can help in choosing the parameters with highest strength to be included in the QMRA model. The real impact of the quality of input parameter can only be assessed after the parameters themselves are actually filled in into the model. Hereby, it might be decided to leave out high quality parameters if they don't fit into the model. To evaluate the impact of the strength of the parameters used in the model, the strengths will be combined with the results of a sensitivity analysis to produce a "Diagnostic Diagram" (van der Sluijs et al., 2005a). Plotting both the sensitivity and the strength of the parameters on this type of diagram will allow identification of the weak parameters in the model, i.e. those parameters with a low strength and having a high contribution to the sensitivity of the output. Describing and critically evaluate the quality of data used in a QMRA is essential step to allow an effective peer-review process. The use of the NUSAP/Pedigree will absolutely improve the decision-makers' awareness of and the confidence in their conclusions from QMRA. The above described process is recommended by the authors and it is advised to implement generally in risk assessment. The process should be regarded as an essential step for quality assurance in (QM)RA.

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